IN THE SPECIFICATION:

Please amend as follows:

Please replace the paragraph on page 12 lines 6-14.

FIGURE 4 depicts the comparison between the murine (SEQ ID NO:2) and human (SEQ ID NO:4) deduced amino acid sequences. The sequence of the human *ob* deduced amino acid sequence was highly homologous to that of mouse. Conservative changes are noted by a dash, and non-conservative changes by an asterisk. The variable glutamine codon is underlined, as is the position of the nonsense mutation in C57BL/6J ob/ob (1J) mice. Overall, there is 83% ~~84%~~ identity at the amino acid level, although only six substitutions were found between the valine at codon 22 (immediately downstream of the signal sequence overage) and the cysteine at position 117.

Please replace the paragraph on page 93 lines 8-20.

Human fat tissue RNA was analyzed on Northern blot, RNA species of similar size to the mouse *ob* gene was detected. Sequencing and analysis of cDNA clones revealed that human *ob* also encodes 167 amino acid polypeptide (Figures 2 and 3). Two classes of cDNA with or without three base pairs deletion were found in human as well (Figure 6). The mouse and human *ob* genes were highly homologous in the predicted coding region, but had only 30% homology in the available 3′ and 5′ untranslated regions. An N-terminal signal sequence was also present in the human *ob* polypeptide. Comparison of the human and mouse *ob* polypeptide sequences showed that the two molecules share an overall 83% ~~84%~~ identity at amino acid level (Figure 4). The N-termini of the mature proteins from both species share even higher homology, with only six ~~four~~ conservative and six ~~three~~ nonconservative amino acid substitutions among the N-terminal 100 amino acid residues.